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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/935,390A

DATE: 11/19/2001

TIME: 15:40:33

Input Set : N:\Crf3\RULE60\09935390A.txt
Output Set: N:\CRF3\11192001\I935390A.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Escobedo, Jaime
6 Quianjin, Hu
7 Garcia, Pablo
8 Williams, Lewis T.
9 Kothakota, Srinivas

C--> 11 (ii) TITLE OF INVENTION: Secreted Human Proteins

13 (iii) NUMBER OF SEQUENCES: 38
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Chiron Corporation
17 (B) STREET: 4560 Horton Street
18 (C) CITY: Emeryville
19 (D) STATE: CA
20 (E) COUNTRY: USA
21 (F) ZIP: 94608-291623 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Diskette
25 (B) COMPUTER: IBM Compatible
26 (C) OPERATING SYSTEM: DOS
27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/935,390A
C--> 31 (B) FILING DATE: 22-Aug-2001
32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/988,671
36 (B) FILING DATE: 1997-12-1138 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: Jane E. R. Potter
40 (B) REGISTRATION NUMBER: 33,332
41 (C) REFERENCE/DOCKET NUMBER: 1369.002

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (510) 923-2718
45 (B) TELEFAX: (510) 655-3542
46 (C) TELEX:

49 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 2063 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear

55 (ix) FEATURE:

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 GAATTGGCA CGAGGCCTCA GTCTTCCAGG GCGGCGGTGG GTGTCCGCTT CTCTCTGCTC 60
59 TTCGACTGCA CCGCACTCGC GCGTGACCCCT GACTCCCCCT AGTCAGCTCA GCGGGCTGCTC 120
60 CATGGCGTGG CGGCGGCGCG AAGCCGGCGT CGGGGCTCGC GGCGTGTGTTGG CTCTGGCGTT 180

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61	GCTCGCCCTG	GCCCTGTGCG	TGCCCCGGGC	CCGGGGCCGG	GCTCTCGAGT	GGTTCTCGGC	240
62	CGTGGTAAAC	ATCGAGTACG	TGGACCCGCA	GACCAACCTG	ACGGTGTGGA	GCGTCTCGGA	300
63	GAGTGGCCGC	TTCGGCGACA	GCTCGCCCAA	GGAGGGCGCG	CATGGCCTGG	TGGGCGTCCC	360
64	GTGGGCGCCC	GGCGGAGACC	TCGAGGGCTG	CGCGCCCGAC	ACCGCGCTTCT	TCGTGCCCGA	420
65	GCCC GGCGGC	CGAGGGGCCG	CGCCCTGGGT	CGCCCTGGTG	GCTCGTGGGG	GCTGCACCTT	480
66	CAAGGACAAG	GTGCTGGTGG	CGGCGCGAG	GAACGCCTCG	GCCGTCGTCC	TCTACAATGA	540
67	GGAGCGCTAC	GGGAACATCA	CCTTGCCCAT	GTCTCACGCG	GGAACAGGAA	ATATAGTGGT	600
68	CATTATGATT	AGCTATCCAA	AAGGAAGAGA	AATTTTGGAG	CTGGTGCAAA	AAGGAATTCC	660
69	AGTAACGATG	ACCATAGGGG	TTGGCACCCG	GCATGTACAG	GAGTTCATCA	GCGGTCAGTC	720
70	TGTGGTGT	TTGGCCATTG	CCTTCATCAC	CATGATGATT	ATCTCGTTAG	CCTGGCTAAT	780
71	ATTTTACTAT	ATACAGCGTT	TCCTATATAC	TGGCTCTCAG	ATTGGAAGTC	AGAGCCATAG	840
72	AAAAGAAACT	AAGAAAGTTA	TTGGCCAGCT	TCTACTTCAT	ACTGTAAAGC	ATGGAGAAAA	900
73	GGGAATTGAT	GTTGATGCTG	AAAATTGTC	AGTGTGTATT	GAAAATTCA	AAGTAAAGGA	960
74	TATTATTAGA	ATTCTGCCAT	GCAAGCATAT	TTTCATAGA	ATATGCATTG	ACCCATGGCT	1020
75	TTTGGATCAC	CGAACATGTC	CAATGTGAA	ACTTGATGTC	ATCAAAGCCC	TAGGATATTG	1080
76	GGGAGAGCCT	GGGGATGTAC	AGGAGATGCC	TGCTCCAGAA	TCTCCTCCTG	GAAGGGATCC	1140
77	AGCTGCAAAT	TTGAGTCTAG	CTTTACCAGA	TGATGACGGA	AGTGTGACA	GCAGTCCACC	1200
78	ATCAGCCTCC	CCTGCTGAAT	CTGAGCCACA	GTGTGATCCC	AGCTTTAAAG	GAGATGCAGG	1260
79	AGAAAATACG	GCATTGCTAG	AAGCCGGCAG	GAGTGACTCT	CGGCATGGAG	GACCCATCTC	1320
80	CTAGCACACG	TGCCCACCTGA	AGTGGCACCA	ACAGAAAGTT	GGCTTGAAC	AAAGGACATT	1380
81	TTATTTTTT	TACTTTAGCA	CATAATTGTT	ATATTGAAA	ATAATGTATA	TTATTTTACC	1440
82	TATTAGATTC	TGATTTGATA	TACAAAGGAC	TAAGATATT	TCTTCTTGAA	GAGACTTTTC	1500
83	GATTAGTCT	CATATATT	TCTACTAAA	TAGAGTGT	ACCATGAAAC	GTGTGTTGCT	1560
84	TCAGACTATT	ACAAAGACAA	CTGGGGCAGG	TACTCTAATA	TAAAGGACAG	GTGGTGTTC	1620
85	TAAATAATTG	GCTGCTATGG	TTCTGTAAAAA	ACCAGTTAAT	TCTATTTTC	AAGGTTTTG	1680
86	GCAAAGCACA	TCAATGTTAG	ACTAGTTGAA	GTGGAATTGT	ATAATTCAAT	TCGATAATTG	1740
87	ATCTCATGGG	CTTCCCTGG	AGGAAAGGTT	TTTTTGTG	TTTTTTTTT	AAGAACATTG	1800
88	AACTTGAAA	CTGAGATGTC	TGTAGCTTT	TTGCCCATCT	GTAGTGTATG	TGAAGATTTC	1860
89	AAAACCTGAG	AGCACTTTT	CTTGTGTTAG	AATTATGAGA	AAGGCAC	ATGACTTTAG	1920
90	GATTGCA	TTTCCCTTTA	TTGCCTCATT	TCTTGTGACG	CTTGTGTTGG	GAGGGAAATC	1980
91	TGTTTATTTT	TTCCCTACAAA	AAAAAAGCTA	AGATTCTATA	TCGAAAAAAA	AAAAA	2040
92	AAAAA	TTCCCTGCGGC	CGC				2063

94 (2) INFORMATION FOR SEQ ID NO: 2:

95 (i) SEQUENCE CHARACTERISTICS:

- 96 (A) LENGTH: 1328 base pairs
- 97 (B) TYPE: nucleic acid
- 98 (C) STRANDEDNESS: single
- 99 (D) TOPOLOGY: linear

100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

102	GAATTCGGCA	CGAGGTAGGC	AAGGGATAAAA	AAGGCACCTA	AGGCCCTTTT	GCAATAAGAA	60
103	GCCAGATGGA	TAAAGGAAGT	GCTGGTCACC	CTGGAGGTGT	ACTGGTTTGG	GGAAGGTCCC	120
104	CGGCC	AGCCCTCTGG	GGAGCCTCAC	CCTGGCTCTC	CCCAC	TCAGCCCTCA	180
105	GGCAGCC	CCACAGGGCC	CCTCTCTGC	CTGGACAGCT	CTGCTGGTCT	CCCCGTCCCC	240
106	TGGAGAAGAA	CAAGGCCATG	GGTCGGCCCC	TGCTGCTGCC	CCTGCTGCTC	CTGCTGCAGC	300
107	CGCCAGCATT	TCTGCAGCCT	GGTGGCTCCA	CAGGATCTGG	TCCAAGCTAC	CTTTATGGGG	360
108	TCACTCAACC	AAAACACCTC	TCAGCCTCCA	TGGGTGGCTC	TGTGGAAATC	CCCTTCTCCT	420
109	TCTATTACCC	CTGGGAGTTA	GCCATAGTT	CCAAACGTGAG	AATATCCTGG	AGACGGGGCC	480
110	ACTTCCACGG	GCAGTCCTC	TACAGCACAA	GGCCGCCTTC	CATTACAAG	GATTATGTGA	540
111	ACCGGCTCTT	TCTGAAC	ACAGAGGGTC	AGGAGAGCGG	CTTCCTCAGG	ATCTCAAACC	600

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112	TGCGGAAGGA	GGACCAGTCT	GTGTATTCT	GCCGAGTCGA	GCTGGACACC	CGGAGATCAG	660
113	GGAGGCAGCA	GTTGCAGTCC	ATCAAGGGGA	CCAAACTCAC	CATCACCCAG	GCTGTCACAA	720
114	CCACCACCA	CTGGAGGCC	AGCAGCACAA	CCACCATAGC	CGGCCTCAGG	GTCACAGAAA	780
115	GCAAAGGCA	CTCAGAATCA	TGGCACCTAA	GTCCTGGACAC	TGCCATCAGG	GTGCAATTGG	840
116	CTGTCGCTGT	GCTAAAAC	GTCATTTGG	GACTGCTGTG	CCTCCTCCTC	CTGTGGTGG	900
117	GGAGAAGGAA	AGGTAGCAGG	GCGCCAAGCA	GTGACTTCTG	ACCAACAGAG	TGTGGGGAGA	960
118	AGGGATGTGT	ATTAGCCCCG	GAGGACGTGA	TGTGAGACCC	GCTTGTGAGT	CCTCCACACT	1020
119	CGTTCCCCAT	TGGCAAGATA	CATGGAGAGC	ACCCCTGAGGA	CCTTTAAAAG	GCAAAGCCGC	1080
120	AAGGCAGAAG	GAGGCTGGGT	CCCTGAATCA	CCGACTGGAG	GAGAGTTACC	TACAAGAGCC	1140
121	TTCATCCAGG	AGCATCCACA	CTGCAATGAT	ATAGGAATGA	GGTCTGAACT	CCACTGAATT	1200
122	AAACCACCTGG	CATTGGGGG	CTGTTTATTA	TAGCAGTGCA	AAGAGTTCC	TTATCCTCCC	1260
123	CAAGGATGGA	AAAATACAAT	TTATTTGCT	TACCATAAAA	AAAAAAAAAA	AAAAAATTCC	1320
124	GGCGCCGC						1328

126 (2) INFORMATION FOR SEQ ID NO: 3:

127 (i) SEQUENCE CHARACTERISTICS:

128 (A) LENGTH: 1689 base pairs
129 (B) TYPE: nucleic acid
130 (C) STRANDEDNESS: single
131 (D) TOPOLOGY: linear

132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

134	GAATTCGGCA	CGAGGGCAAG	ATTCGATACA	AAACCAATGA	ACCTGTGTGG	GAGGAAAAC	60
135	TCACTTCTT	CATTACAAT	CCCAAGCGCC	AGGACCTTGA	AGTTGAGGTC	AGAGACGAGC	120
136	AGCACCACTG	TTCCCTGGGG	AACCTGAAGG	TCCCCCTCAG	CCAGCTGCTC	ACCACTGAGG	180
137	ACATGACTGT	GAGCCAGCGC	TTCCAGCTCA	GTAACTCGGG	TCCAAACAGC	ACCATCAAGA	240
138	TGAAGATTGC	CCTGCGGGTG	CTCCATCTCG	AAAAGCGAGA	AAGGCCTCCA	GACCACCAAC	300
139	ACTCAGCTCA	AGTCAAACGT	CCCTCTGTGT	CCAAAGAGGG	GAGGAAAACA	TCCATCAAAT	360
140	CTCATATGTC	TGGGTCTCCA	GGCCCTGGTG	GCAGCAACAC	AGCTCCATCC	ACACCAGTCA	420
141	TTGGGGCAG	TGATAAGCCT	GGTATGGAAG	AAAAGGCCA	GCCCCCTGAG	GCCGGCCCTC	480
142	AGGGGCTGCA	CGACCTGGGC	AGAAGCTCCT	CCAGCCTCCT	GGCCTCCCCA	GGCCACATCT	540
143	CAGTCAGGA	GCCGACCCCC	AGCATCCCT	CGGACATCTC	GCTGCCCATC	GCCACCCAGG	600
144	AGCTCGGGCA	AAGGCTGAGG	CAGCTGAAA	ACGGGACGAC	CCTGGGACAG	TCTCCACTGG	660
145	GGCAGATCCA	GCTGACCATC	CGGCACAGCT	CGCAGAGAAA	CAAGCTTATC	GTGGTCGTGC	720
146	ATGCCTGAG	AAACCTCATT	GCCTTCTCTG	AAGACGGCTC	TGACCCCTAT	GTCCGCATGT	780
147	ATTATTAC	AGACAAGAGG	CGGTCAGGAA	GGAGGAAAAC	ACACGTGTCA	AAGAAAACAT	840
148	TAAATCCAGT	GTGGATCAA	AGCTTTGATT	TCAGTGTTC	GTTACCAAGAA	GTGCAGAGGA	900
149	GAACGCTCGA	CGTTGCCGTG	AAGAACAGTG	GGGGCTTCCT	GTCCAAAGAC	AAAGGGCTCC	960
150	TTGGCAAAGT	ATTGGTTGCT	CTGGCATCTG	AAGAACTTGC	CAAAGGCTGG	ACCCAGTGGT	1020
151	ATGACCTCAC	GGAAAGATGGG	ACGAGGCC	AGGCATGAC	ATAGCCCGAG	CAGGCAGGAG	1080
152	GCGTCCTCTT	CAGCGTAGCT	CTCCACCTCT	ACCCGGAACA	CACCCCTCTCA	CAGACGTACC	1140
153	AATGTTATT	TTATAATTTC	ATGGATTAG	TTATACATAC	CTTAATAGTT	TTATAAAATT	1200
154	GTTGACATT	CAGGCAAATT	TGGCCAATAT	TATCATTGAA	TTTTCTGTGT	TGGATTTCC	1260
155	CTAGGATTTC	GCCAGTTCT	ACAACGTGCA	GTAGGGCGGC	GGTAGCTCTT	GTGTCTGTGG	1320
156	ACTCTGCTCA	GCTGTGTCCG	TAGGAGTCGG	ATGTGTCTGT	GCTTTATTAT	GGCCTTGT	1380
157	ATATATCACT	GAGGTATACT	ATGCCATGTA	AATAGACTAT	TTTTTATAAT	CTTAACATGC	1440
158	TGGTTAAAT	TCAGAAGGAA	ATAGATCAAG	GAAATATATA	TATTTCTTC	AAAAACTTAT	1500
159	TAAATTCGTG	TGACAAATAA	TCATTTCAT	CTTGGCAGCA	AAAAGTTCTC	AGTGACCTAT	1560
160	TTTGTGGTGT	TTCTTTTGA	AAAGAAAAGC	TGAAATATTA	TTAAATGCTA	GTATGTTCT	1620
161	GCCCATTATG	AAAGATGAAA	TAAGTATTC	AAAATATTA	AAAAAAAAAA	AAAAAATTCC	1680
162	TGCGGCCGC						1689

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165 (2) INFORMATION FOR SEQ ID NO: 4:

166 (i) SEQUENCE CHARACTERISTICS:

167 (A) LENGTH: 1505 base pairs
168 (B) TYPE: nucleic acid
169 (C) STRANDEDNESS: single
170 (D) TOPOLOGY: linear

171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

173	GAATTGGCA CGAGGAGCAG ATCTGCAAGA GTTTCGTTTA TGGAGGCTGC TTGGGCAACA	60
174	AGAACAACTA CCTTCGGGAA GAAGAGTGCA TTCTAGCCTG TCGGGGTGTG CAAGGTGGC	120
175	CTTTGAGAGG CAGCTCTGGG GCTCAGCGA CTTTCCCCCA GGGCCCCCTCC ATGGAAAGGC	180
176	GCCATCCAGT GTGCTCTGGC ACCTGTCAAGC CCACCCAGTT CCGCTGCAGC AATGGCTGCT	240
177	GCATCGACAG TTTCTGGAG TGTGACGACA CCCCCAAGTG CCCCAGCGCC TCCGACGAGG	300
178	CTGCCTGTGA AAAATACACG AGTGGCTTTG ACGAGCTCCA GCGCATCCAT TTCCCCAGCG	360
179	ACAAAGGGCA CTGCGTGGAC CTGCCAGACA CAGGACTCTG CAAGGAGAGC ATCCCGCGCT	420
180	GGTACTACAA CCCCTTCAGC GAACACTGCG CCCGTTTAC CTATGGTGGT TGTACGGCA	480
181	ACAAGAACAA CTTTGAGGAA GAGCAGCAGT GCCTCGAGTC TTGTCGCGGC ATCTCCAAGA	540
182	AGGATGTGTT TGGCCTGGAG CGGGAAATCC CCATTCCCAG CACAGGCTCT GTGGAGATGG	600
183	CTGTCGAGT GTTCCTGGTC ATCTGCATTG TGGTGGTGGT AGCCATCTTG GGTACTGCT	660
184	TCTTCAAGAA CCAAGAGAAAG GACTTCCACG GACACCACCA CCACCCACCA CCCACCCCTG	720
185	CCAGCTCCAC TGTCTCCACT ACCGAGGACA CGGAGCACCT GGTCTATAAC CACACCACGC	780
186	GGCCCCCTTG AGCCTGGGTC TCACCGGCTC TCACCTGGCC CTGCTCCTG CTTGCCAAGG	840
187	CAGAGGCTG GGCTGGGAAA AACTTTGGAA CCAGACTCTT GCCTGTTCC CAGGCCACT	900
188	GTGCCTCAGA GACCAGGGCT CCAGCCCTC TTGGAGAAGT CTCAGCTAAG CTCACGTCT	960
189	GAGAAAGCTC AAAGGTTTGG AAGGAGCAGA AAACCCCTTGG GCCAGAAGTA CCAGACTAGA	1020
190	TGGACCTGCC TGCACTAGGAG TTTGGAGGAA GTTGGAGTTT TGTTTCCCT GTCAAAGCT	1080
191	GCCTGTCCCT ACCCCATGGT GCTAGGAAGA GGAGTGGGGT GGTGTCAAGAC CCTGGAGGCC	1140
192	CCAACCCCTGT CCTCCCGAGC TCCTCTCCA TGCTGTGCGC CCAGGGCTGG GAGGAAGGAC	1200
193	TTCCCTGTGT AGTTTGTGCT GTAAAGAGTT GCTTTTTGTT TATTTAATGC TGTGGCATGG	1260
194	GTGAAGAGGA GGGGAAGAGG CCTGTTGGC CTCTCTATCC TCTCTCCTC TTCCCCCAAG	1320
195	ATTGAGCTCT CTGCCCTTGA TCAGCCCCAC CCTGGCCTAG ACCAGCAGAC AGAGCCAGGA	1380
196	GAAGCTCAGC TGCATTCCGC AGCCCCCACC CCCAAGGTTT TCCAACATCA CAGCCCAGCC	1440
197	CGCCCACTGG GTAATAAAAG TGGTTGTGG AAAAAAAA AAAAAAAA AAGTCCTGCG	1500
198	GCCGC	1505

200 (2) INFORMATION FOR SEQ ID NO: 5:

201 (i) SEQUENCE CHARACTERISTICS:

202 (A) LENGTH: 2002 base pairs
203 (B) TYPE: nucleic acid
204 (C) STRANDEDNESS: single
205 (D) TOPOLOGY: linear

206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

208	GAATTGGCA CGAGGGCCAT GGCGGGCTA TCCCGCGGGT CCGCGCGCGC ACTGCTCGCC	60
209	GCCCTGCTGG CGTCGACGCT GTTGGCGCTG CTCGTGTGCG CCGCGCGGGG TCGCGGGCGC	120
210	CGGGACCACG GGGACTGGGA CGAGGCCCTCC CGGCTGCCGC CGCTACCAACC CCGCGAGGAC	180
211	CGGGCGCGCG TGGCCCGCTT CGTGACGCAC GTCTCCGACT GGGGCGCTCT GGCCACCATC	240
212	TCCACGCTGG AGGCGGTGCG CGGCCGCC TCGCGGACG TCCTCTCGCT CAGCGACGGG	300
213	CCCCCGGGCG CGGGCAGCGG CGTGCCTAT TTCTACCTGA GCCCGCTGCA GCTCTCCGTG	360
214	AGCAACCTGC AGGAGAATCC ATATGCTACA CTGACCATGA CTTTGGACAA GACCAACTTC	420
215	TGCAAGAAC ATGGATTGTA TCCACAAAGT CCCCTTTGTG TTCACATAAT GCTGTCAAGA	480
216	ACTGTACCA AGGTGAATGA AACAGAAATG GATATTGCAA AGCATTGTT ATTCAATTGCA	540

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217	CACCCCTGAGA	TGAAAACCTG	GCCTTCCAGC	CATAATTGGT	TCTTTGCTAA	GTTGAATATA	600
218	ACCAATATCT	GGGTCCCTGGA	CTACTTTGGT	GGACCAAAAA	TCGTGACACC	AGAAGAATAT	660
219	TATAATGTCA	CAGTTCAGTG	AAGCAGACTG	TGGTGAATT	AGCAACACTT	ATGAAGTTTC	720
220	TTAAAGTGGC	TCATACACAC	TTAAAAGGCT	TAATGTTTCT	CTGGAAAGCG	TCCCAGAATA	780
221	TTAGCCAGTT	TTCTGTCA	TGCTGGTTG	TTTGCTTGCT	TGTTTACTTG	CTTGTGTTACC	840
222	AATAGAGTTG	ACCTGTTATT	GGATTTCTG	GAAGATGTGG	TAGCTACTTT	TTTCCTATTT	900
223	TGAAGCCATT	TTCTGTAGAGA	AATATCCTTC	ACTATAATCA	AATAAGTTT	GTCCCACATCAA	960
224	TTCCAAAGAT	GTTCAGTG	GTGCTCTTGA	AGAGGAATGA	GTACCAAGTTT	TAATTGCCCC	1020
225	ATTGGCATT	GAAGGTAGTT	GAGTATGTGT	TCTTATTCC	TAGAAGCCAC	TGTGCTTGGT	1080
226	AGAGTGCATC	ACTCACCAC	GCTGCCCTT	GAGCTGCC	AGCCTGGTGC	AAAAGGATTG	1140
227	GCCCCCATTA	TGGTCTTCT	GAATAATCT	TGCCAACAGA	GACAAACAA	GATGAAACTC	1200
228	AGATGGAGCT	TCCTACTCAT	GTTGATTAT	GTCTCACAA	CCTGGGTATT	GTAAATTCAA	1260
229	CATAGGGTGA	AACTATTCT	GATAAAGAAC	TTTGAAAAA	CTTTTATAC	TCTAAAGTGA	1320
230	TACTCAGAAC	AAAAGAAAGT	CATAAAACTC	CTGAATTAA	TTTCCCCACC	TAAGTCGAGA	1380
231	CACTTATTC	AAAACACATG	TGCACACAGA	TTATTTTTG	GCTCCAAAC	TGGATTGCAA	1440
232	AAGAAAGAGG	AGAGATATT	TGTGTGTTCC	TGGTATTCTT	TTATAAGTAA	AGTTACCCAG	1500
233	GCATGGACCA	GCCTCAGCCA	GGGACAAAAT	CCCCCTCCAA	ACCACTCTCC	ACAGCTTTT	1560
234	AAAAATACTT	CTACTCTTAA	CAATTACCTA	AGGTTCC	AAACCCCCCC	AACTCTTAAT	1620
235	AGCTCTAGT	GCTGCTACAA	TCTAAGTCAG	GTCAACCAAG	GGAAGAGAAC	ATGGCATTAA	1680
236	AAGAACATCA	TCTTCAGAAC	AGAACAGACT	AATATTATTA	CCCATATACA	TGATTTCAGA	1740
237	AGATGACATA	AGATTCCCT	TAAGAGGAA	ATGTCAGGAA	TCAAGCCACT	GAATCCTTAA	1800
238	AGAGAAAAGT	TGAATATGAG	TCATTGTGTC	TGAAAAC	AAAGTGAAC	TAAC	1860
239	CCAGCAAACA	GGTTCTGTT	AAGAAAAATA	ATTTACTA	AATTTAGTAA	AATGGACTTC	1920
240	TTATTCAAAG	CATCAATAAT	TAAGAATT	ATTTAAAAA	AAAAAAA	AAAAAAA	1980
241	AAAAAAAAT	TCTCGCGGCC	GC				2002

243 (2) INFORMATION FOR SEQ ID NO: 6:

244 (i) SEQUENCE CHARACTERISTICS:

- 245 (A) LENGTH: 1322 base pairs
- 246 (B) TYPE: nucleic acid
- 247 (C) STRANDEDNESS: single
- 248 (D) TOPOLOGY: linear

249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

251	GAATTCCGGCA	CGAGGGCCAC	GACTCTGCTG	GCATTTCTTC	TATAGCCACT	GGAATCTGAT	60
252	CCTGATTGTC	TTCCACTACT	ACCAGGCCAT	CACCACTCCG	CCTGGGTACC	CACCCAGGG	120
253	CAGGAATGAT	ATCGCCACCG	TCTCCATCTG	TAAGAAGTGC	ATTTACCCCA	AGCCAGCCCG	180
254	AACACACCAC	TGCAGCATCT	GCAACAGGTG	TGTGCTGAAG	ATGGATCACC	ACTGCCCTG	240
255	GCTAAACAA	TGTGTGGGCC	ACTATAACCA	TCGGTACTTC	TTCTCTTCT	GCTTTTCCAT	300
256	GACTCTGGGC	TGTGTCTACT	GCAGCTATGG	AAGTTGGAC	CTTTTCCGGG	AGGCTTATGC	360
257	TGCCATTGAG	AAAATGAAAC	AGCTCGACAA	GAACAAACTA	CAGGCGGTTG	CCAACCAGAC	420
258	TTATCACCA	ACCCACCAC	CCACCTCTC	CTTTCGAGAA	AGGATGACTC	ACAAGAGTCT	480
259	TGTCTACCTC	TGTTCCCTGT	GCAGTTCTGT	GGCACTTGCC	CTGGGTGCC	TAACTGTATG	540
260	GCATGCTGTT	CTCATCAGTC	GAGGTGAGAC	TAGCATCGAA	AGGCACATCA	ACAAGAAGGA	600
261	GAGACGTCGG	CTACAGGCCA	AGGGCAGAGT	ATTAGGAAT	CCTTACA	ACGGCTGCTT	660
262	GGACAACTGG	AAGGTATTCC	TGGGTGTTGA	TACAGGAAGG	CACTGGCTTA	CTCGGGTGCT	720
263	CTTACCTTCT	ACTCACTTGC	CCCATGGAA	TGGAATGAGC	TGGGAGCCCC	CTCCCTGGGT	780
264	GACTGCTCAC	TCAGCCTCTG	TGATGGCAGT	GTGAGCTGGA	CTGTGTCAGC	CACGACTCGA	840
265	GCACTCATTC	TGCTCCCTAT	GTTATTCAA	GGGCCTCCAA	GGGCAGCTTT	TCTCAGAATC	900
266	CTTGATCAA	AAGAGCCAGT	GGGCCTGCCT	TAGGGTACCA	TGCAGGACAA	TTCAAGGACC	960
267	AGCCTTTTA	CCACTGCGAGA	AGAAAGACAC	AATGTGGAGA	AATCTTAGGA	CTGACATCCC	1020

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L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:56 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:714 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:864 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:931 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:1032 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:1081 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:1179 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:1237 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:1289 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:1350 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:1408 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:1490 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:1548 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:1630 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:1704 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:1768 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:1820 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37
L:1920 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38